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## What is claimed is:

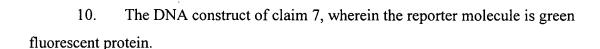
- An isolated Ikaros transcriptional control region comprising one or more Ikaros regulatory element.
- 2. The Ikaros transcriptional control region of claim 1, comprising all or a functional fragment of a promoter of the  $\beta$  cluster.
- 3. The Ikaros regulatory control region of claim 1, comprising all or a functional fragment of a promoter of the y cluster. 10
  - 4. The Ikaros regulatory control region of claim 2, further comprising all or a functional fragment of a promoter of the y cluster.
  - 5. The Ikaros regulatory control region of any of claims 2, 3 or 4, further comprising one or more Ikaros regulatory element from the  $\alpha$  cluster, the  $\epsilon$  cluster, the  $\eta$ cluster or the  $\theta$  cluster.
  - 6. The Ikaros regulatory control region of claim 4, further comprising the  $\varepsilon$ cluster or a portion thereof.
  - 7. A DNA construct comprising an Ikaros transcriptional control region of claim 1 and a sequence encoding a reporter molecule.
  - 8. The DNA construct of claim 7, wherein the reporter molecule is a reporter molecule which can luminesce or fluoresce.
    - 9. The DNA construct of claim 7, wherein the reporter molecule is selected from a beta-galactosidase gene, a luciferase gene, a green fluorescent protein gene, an alkaline phosphatase gene, a horseradish peroxidase gene, and a chloramphenicol acetyl transferase gene.

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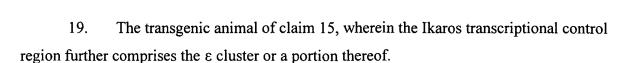
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- 11. A transgenic animal, or cell or tissue therefrom, comprising a transgene includes an Ikaros transcriptional control region operably linked to a sequence which is functionally unrelated to the Ikaros gene.
  - 12. The transgenic animal of claim 11, wherein the animal is a rodent.
  - 13. The transgenic animal of claim 12, wherein the rodent is a mouse.
- 14. The transgenic animal of claim 11, wherein the Ikaros transcriptional control region includes one or more Ikaros regulatory element.
- 15. The transgenic animal of claim 11, wherein the Ikaros transcriptional control region comprises the  $\beta$  cluster or a functional fragment of the promoter of the  $\beta$  cluster.
- 16. The transgenic animal of claim 11, wherein the Ikaros transcriptional control region comprises the  $\gamma$  cluster or a functional fragment of the promoter of the  $\gamma$  cluster.
- 17. The transgenic animal of claim 15, wherein the Ikaros transcriptional control region further comprises the  $\gamma$  cluster or a functional fragment of the promoter of the  $\gamma$  cluster.
- 18. The transgenic animal of any of claims 14, 15, or 16, wherein the Ikaros transcriptional control region further comprises one or more Ikaros regulatory element from the  $\alpha$  cluster or a portion thereof, the  $\epsilon$  cluster or a portion thereof, or the  $\theta$  cluster or a portion thereof.

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- The transgenic animal of claim 19, wherein the Ikaros transcriptional control
  region comprises a portion of the ε cluster.
  - 21. The transgenic animal of claim 11, wherein the sequence functionally unrelated to the Ikaros gene encodes a reporter molecule.
- The transgenic animal of claim 21, wherein the reporter molecule is a reporter molecule which can luminesce or fluoresce.
  - 23. The transgenic animal of claim 21, wherein the sequence encoding the reporter molecule is selected from a beta-galactosidase gene, a luciferase gene, a green fluorescent protein gene, an alkaline phosphatase gene, a horseradish peroxidase gene, and a chloramphenicol acetyl transferase gene.
  - 24. The transgenic animal of claim 21, wherein the reporter molecule is green fluorescent protein or a variant thereof.
  - 25. The transgenic animal of claim 24, wherein the reporter molecule is a variant of green fluorescent protein.
  - 26. The transgenic animal of claim 25, wherein the variant of green fluorescent protein is selected from the group consisting of EGFP, EBFP, EYFP, d2EGFP, ECFP, and GFPuv.
    - 27. The transgenic animal of claim 11, wherein the genome of the animal further comprises an alteration by disrupting at least one exon of the endogenous Ikaros gene.

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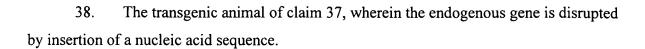
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- 28. The transgenic animal of claim 27, wherein the endogenous Ikaros gene is disrupted by insertion of a nucleic acid sequence.
- 29. The transgenic animal of claim 28, wherein the insertion results in any of an inversion, deletion, translocation, or reciprocal translocation.
  - 30. The transgenic animal of claim 28, wherein the insertion is in or alters the sequence, expression, or splicing of one or more of the following exons: exon 1/2, exon 3, exon 4, exon 5, exon 6, and exon 7.
  - 31. The transgenic animal of claim 28, wherein the insertion is in or alters the sequence, expression, or splicing of a DNA binding domain of the Ikaros gene.
  - 32. The transgenic animal of claim 28, wherein the insertion results in a deletion of portions of exon 3 and exon 4.
  - 33. The transgenic animal of claim 28, wherein the animal is heterozygous for the insertion.
  - 34. The transgenic animal of claim 28, wherein the animal is homozygous for the insertion.
  - 35. The transgenic animal of claim 28, wherein the insertion is in a domain involved in transcriptional activation or in dimerization.
    - 36. The transgenic animal of claim 28, wherein the insertion is in exon 7.
  - 37. The transgenic animal of claim 11, wherein the genome of the animal further comprises an alteration by disrupting at least one exon of the endogenous gene encoding a protein involved in hematopoiesis.

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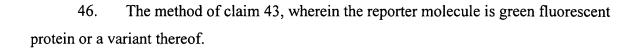


- 39. The transgenic animal of claim 38, wherein the endogenous gene encodes Helios.
  - 40. The transgenic animal of claim 38, wherein the endogenous gene encodes Aiolos.
- 10 41. The transgenic animal of claim 38, wherein the insertion results in any of an inversion, deletion, translocation, or reciprocal translocation.
  - 42. A method of evaluating the development of a component or a cell lineage of the immune system, comprising:

providing a transgenic animal of claim 11 or claim 37, or a cell or tissue therefrom; and

monitoring expression of the protein unrelated to Ikaros.

- 43. The method of claim 42, wherein the sequence functionally unrelated to the Ikaros gene encodes a reporter molecule.
- 44. The method of claim 43, wherein the reporter molecule is a reporter molecule which can luminesce or fluoresce.
- 25 45. The method of claim 43, wherein the sequence encoding the reporter molecule is selected from a beta-galactosidase gene, a luciferase gene, a green fluorescent protein gene, an alkaline phosphatase gene, a horseradish peroxidase gene, and a chloramphenicol acetyl transferase gene.



- 47. The method of claim 46, wherein the reporter molecule is a variant of green fluorescent protein.
  - 48. The method of claim 47, wherein the variant of green fluorescent protein is selected from the group consisting of EGFP, EBFP, EYFP, d2EGFP, ECFP, and GFPuv.
- 10 49. The method of claim 43, wherein hematopoietic development is evaluated in a living animal.
  - 50. The method of claim 49, wherein hematopoietic development is evaluated by detecting a fluorescent signal on the live animal.